

results of BLAST

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1084307128-16635-68711394475.BLASTQ3

Query=

(191 letters) *SEQ ID NO: 206*

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

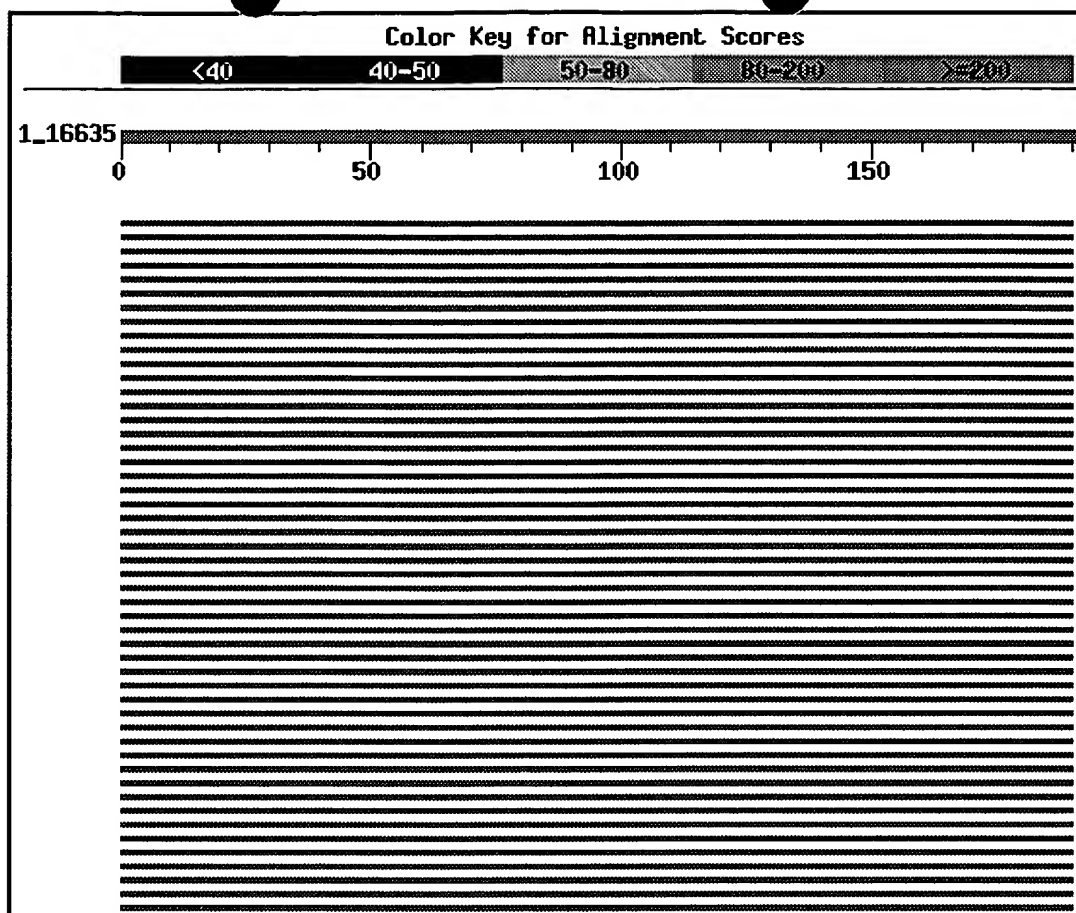
1,798,171 sequences; 593,787,773 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:		Score (bits)	E Value
gi 2326455 emb CAA72801.1	polyprotein [Hepatitis C virus t...	293	2e-78
gi 3550763 dbj BAA32666.1	polyprotein [Hepatitis C virus]	291	4e-78
gi 3550761 dbj BAA32665.1	polyprotein [Hepatitis C virus]	285	5e-76
gi 3550765 dbj BAA32667.1	polyprotein [Hepatitis C virus]	285	5e-76
gi 600265 dbj BAA13617.1	core, env and part of E2/NS1 [Hep...	282	2e-75
gi 1765877 dbj BAA13620.1	core, env and part of E2/NS1 [He...	282	3e-75
gi 1765873 dbj BAA13618.1	core, env and part of E2/NS1 [He...	281	5e-75
gi 1765875 dbj BAA13619.1	core, env and part of E2/NS1 [He...	280	8e-75
gi 2252490 emb CAA72338.1	HCV polyprotein [Hepatitis C vir...	280	9e-75
gi 3550759 dbj BAA32664.1	polyprotein [Hepatitis C virus]	280	1e-74
gi 1765881 dbj BAA13622.1	core, env and part of E2/NS1 [He...	280	1e-74
gi 7650248 gb AAF65955.1	polyprotein [Hepatitis C virus]	280	1e-74
gi 464178 dbj BAA03581.1	polyprotein [Hepatitis C virus]	279	2e-74
gi 1765885 dbj BAA13624.1	core, env and part of E2/NS1 [He...	279	2e-74
gi 1765879 dbj BAA13621.1	core, env and part of E2/NS1 [He...	279	2e-74
gi 1765887 dbj BAA13625.1	core, env and part of E2/NS1 [He...	279	3e-74
gi 7650256 gb AAF65959.1	polyprotein [Hepatitis C virus]	278	3e-74
gi 482138 pir S40770	genome polyprotein - hepatitis C viru...	278	4e-74
gi 2327073 gb AAB67037.1	polyprotein [Hepatitis C virus st...	278	4e-74
gi 471117 dbj BAA01728.1	polyprotein precursor [Hepatitis ...	278	4e-74
gi 130461 sp P27958 POLG HCVH	Genome polyprotein [Contains:...	278	4e-74
gi 8926245 gb AAF81759.1	polyprotein [Hepatitis C virus]	278	4e-74
gi 130455 sp P26664 POLG HCV1	Genome polyprotein [Contains:...	278	4e-74

gi 14532245 gb AAK66554.1 	HCV type 1a/1b chimera polyprote...	278	5e-74
gi 2327071 gb AAB67036.1 	polyprotein [Hepatitis C virus st...	278	5e-74
gi 22129793 ref NP_671491.1 	polyprotein [Hepatitis C virus...	278	5e-74
gi 14532251 gb AAK66557.1 	HCV type 1a/1b chimera mutant po...	278	5e-74
gi 2327075 gb AAB67038.1 	polyprotein [Hepatitis C virus st...	278	5e-74
gi 9930557 gb AAG02099.1 	polyprotein [Hepatitis C virus]	278	5e-74
gi 3098655 gb AAC15732.1 	polyprotein [Hepatitis C virus]	277	6e-74
gi 15529111 gb AAK97744.1 	polyprotein [Hepatitis C virus]	277	6e-74
gi 1944376 dbj BAA19625.1 	unnamed protein product [Hepatit...	277	7e-74
gi 1009261 dbj BAA07091.1 	core, env and part of E2/NS1 [He...	277	7e-74
gi 3098644 gb AAC15727.1 	polyprotein [Hepatitis C virus]	277	7e-74
gi 5918961 gb AAD56196.1 	polyprotein [Hepatitis C virus]	277	8e-74
gi 2943784 dbj BAA25076.1 	polyprotein [Hepatitis C virus]	277	8e-74
gi 7650246 gb AAF65954.1 	polyprotein [Hepatitis C virus]	277	8e-74
gi 7650240 gb AAF65951.1 	polyprotein [Hepatitis C virus]	277	9e-74
gi 5420377 emb CAB46677.1 	polyprotein [Hepatitis C virus t...	277	9e-74
gi 5918963 gb AAD56197.1 	polyprotein [Hepatitis C virus]	277	9e-74
gi 7650244 gb AAF65953.1 	polyprotein [Hepatitis C virus]	277	9e-74
gi 7650224 gb AAF65943.1 	polyprotein [Hepatitis C virus]	277	1e-73
gi 7650234 gb AAF65948.1 	polyprotein [Hepatitis C virus]	277	1e-73
gi 7341103 gb AAF61205.1 	polyprotein [Hepatitis C virus]	276	1e-73
gi 1814086 dbj BAA09072.1 	polyprotein [Hepatitis C virus]	276	1e-73
gi 7650252 gb AAF65957.1 	polyprotein [Hepatitis C virus]	276	1e-73
gi 1814089 dbj BAA09076.1 	polyprotein [Hepatitis C virus]	276	1e-73
gi 1765868 dbj BAA13615.1 	core, env and part of E2/NS1 [He....	276	1e-73
gi 1009263 dbj BAA07092.1 	core, env and part of E2/NS1 [He...	276	1e-73
gi 7650226 gb AAF65944.1 	polyprotein [Hepatitis C virus]	276	2e-73
gi 221607 dbj BAA01583.1 	polyprotein precursor [Hepatitis ...	276	2e-73
gi 1009271 dbj BAA07271.1 	core, env and part of E2/NS1 [He...	276	2e-73
gi 1765870 dbj BAA13616.1 	core, env, and part of E2/NS1 [He...	275	2e-73
gi 1009257 dbj BAA07089.1 	core, env, and part of E2/NS1 [He...	275	3e-73
gi 1009259 dbj BAA07090.1 	core, env and part of E2/NS1 [He...	275	3e-73
gi 1765866 dbj BAA13614.1 	core, env and part of E2/NS1 [He...	274	5e-73
gi 3523057 dbj BAA32652.1 	polyprotein [Hepatitis C virus]	274	5e-73
gi 3523059 dbj BAA32653.1 	polyprotein [Hepatitis C virus]	274	6e-73
gi 1009265 dbj BAA07093.1 	core, env and part of E2/NS1 [He...	273	9e-73
gi 3523055 dbj BAA32651.1 	polyprotein [Hepatitis C virus]	273	1e-72
gi 1066618 gb AAC42193.1 	core protein	273	1e-72
gi 1765891 dbj BAA13627.1 	core, env and part of E2/NS1 [He...	273	1e-72
gi 601937 dbj BAA06739.1 	core, env and part of E2/NS1 [Hep...	272	2e-72
gi 1765883 dbj BAA13623.1 	core, env and part of E2/NS1 [He...	272	2e-72
gi 540813 pir PN0677	hypothetical protein 787 - hepatitis ...	271	6e-72
gi 1765889 dbj BAA13626.1 	core, env and part of E2/NS1 [He...	270	1e-71
gi 1009269 dbj BAA07095.1 	core, env and part of E2/NS1 [He...	270	1e-71
gi 1372958 gb AAB02127.1 	polyprotein [Hepatitis C virus]	270	2e-71
gi 2580421 dbj BAA23132.1 	polyprotein [Hepatitis C virus]	269	2e-71
gi 410168 gb AAA20154.1 	structural region	269	3e-71
gi 1009255 dbj BAA07088.1 	polyprotein [Hepatitis C virus]	268	3e-71
gi 22212866 gb AAM94419.1 	polyprotein [Hepatitis C virus]	268	4e-71
gi 37961928 gb AAP69953.1 	polyprotein [Hepatitis C virus]	268	4e-71
gi 93949 pir S12707	genome polyprotein - hepatitis C virus...	268	6e-71
gi 1009267 dbj BAA07094.1 	core, env, and part of E2/NS1 [He...	268	6e-71
gi 13344959 gb AAK19133.1 	polyprotein precursor [Hepatitis...	266	2e-70
gi 1066620 gb AAC42194.1 	core protein	266	2e-70
gi 13344949 gb AAK19128.1 	polyprotein precursor [Hepatitis...	265	3e-70
gi 23328866 gb AAC42195.2 	core protein [Hepatitis C virus]	265	4e-70
gi 474978 dbj BAA03730.1 	polyprotein [Hepatitis C virus]	265	4e-70
gi 1181855 gb AAA86917.1 	polyprotein	265	4e-70
gi 13344947 gb AAK19127.1 	polyprotein precursor [Hepatitis...	265	4e-70
gi 464172 dbj BAA03732.1 	polyprotein [Hepatitis C virus]	265	5e-70

gi 13344953 gb AAK19130.1 	polyprotein precursor [Hepatitis...	264	6e-70
gi 13344951 gb AAK19129.1 	polyprotein precursor [Hepatitis...	264	6e-70
gi 13344963 gb AAK19135.1 	polyprotein precursor [Hepatitis...	263	9e-70
gi 13344969 gb AAK19138.1 	polyprotein precursor [Hepatitis...	263	1e-69
gi 13344961 gb AAK19134.1 	polyprotein precursor [Hepatitis...	263	1e-69
gi 13344967 gb AAK19137.1 	polyprotein precursor [Hepatitis...	263	1e-69
gi 13344965 gb AAK19136.1 	polyprotein precursor [Hepatitis...	263	1e-69
gi 221512 dbj BAA00705.1 	structural protein [Hepatitis C v...	263	1e-69
gi 1066604 gb AAC42186.1 	core protein	263	2e-69
gi 532381 gb AAA21037.1 	polyprotein	263	2e-69
gi 913996 gb AAB34375.1 	polyprotein [Hepatitis C virus]	262	3e-69
gi 974347 gb AAB40038.1 	core protein [Hepatitis C virus ty...	260	9e-69
gi 1066606 gb AAC42187.1 	core protein	260	1e-68
gi 329736 gb AAA98989.1 	capsid and envelope:x proteins	259	2e-68
gi 1369771 gb AAB02117.1 	core protein	259	2e-68
gi 38147542 gb AAR12079.1 	polyprotein [Hepatitis C virus]	258	4e-68
gi 1246371 dbj BAA09974.1 	polyprotein [Hepatitis C virus]	251	4e-66

Alignments

Get selected sequences

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☐ >[gi|2326455|emb|CAA72801.1|](#) polyprotein [Hepatitis C virus type 6a]
Length = 3018

Score = 293 bits (749), Expect = 2e-78
Identities = 144/191 (75%), Positives = 145/191 (75%)

```

Query: 1  MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MSTLPKPQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRKGPRLGVRATRKTSESRQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKARQPQGRHWAQPGYPWPPLYG+EGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61  RRQPIPKARQPQGRHWAQPGYPWPPLYGSEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDTLTCGFADLM YI                      RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMWYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

```

☐ >[gi|3550763|dbj|BAA32666.1|](#) polyprotein [Hepatitis C virus]
Length = 3016

Score = 291 bits (745), Expect = 4e-78
Identities = 144/191 (75%), Positives = 145/191 (75%)

```

Query: 1  MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MSTLPKPQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

```

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRNLG
 Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI RAIEDGINYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA
 Sbjct: 181 LLSCLTTPASA 191

☐ >gi|3550761|dbj|BAA32665.1| polyprotein [Hepatitis C virus]
 Length = 3013

Score = 285 bits (728), Expect = 5e-76
 Identities = 140/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MSTLPKPQ P DVKFPGGGQIV ATRKTSESRQPRG
 Sbjct: 1 MSTLPKPQKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKAR+ GR WAQPGYPWPLYGNEGCGW GWLLSPRGSRPHWGPNDPRRRSRNLG
 Sbjct: 61 RRQPIPKARRQTGRTWAQPGYPWPLYGNEGCGWGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAVEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA
 Sbjct: 181 LLSCLTTPASA 191

☐ >gi|3550765|dbj|BAA32667.1| polyprotein [Hepatitis C virus]
 Length = 3015

Score = 285 bits (728), Expect = 5e-76
 Identities = 140/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MSTLPKPQ P DVKFPGGGQIV ATRKTSESRQPRG
 Sbjct: 1 MSTLPKPQKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP GR W QPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPIGRSWGQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCG ADLMGYI RAIEDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGLADLMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA
 Sbjct: 181 LLSCLTTPASA 191

☐ >gi|600265|dbj|BAA13617.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 282 bits (722), Expect = 2e-75
Identities = 144/191 (75%), Positives = 145/191 (75%)

```
Query: 1  MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MSTLPPKQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTLPPKQPKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRNLG
Sbjct: 61  RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDTLTCGFADLMGYI                      RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191
```

☐ >gi|1765877|dbj|BAA13620.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 282 bits (721), Expect = 3e-75
Identities = 143/191 (74%), Positives = 144/191 (75%)

```
Query: 1  MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MSTLPPKQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTLPPKQPKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKARQP GRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61  RRQPIPKARQPTGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDT+TCGFADLMGYI                      R IEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTITCGFADLMGYIPVLGAPLGGVAAALAHGVRIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191
```

☐ >gi|1765873|dbj|BAA13618.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 281 bits (719), Expect = 5e-75
Identities = 143/191 (74%), Positives = 144/191 (75%)

```
Query: 1  MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MSTLPPKQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
```

Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG

Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRALEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTP SA

Sbjct: 181 LLSCLTTPASA 191

☐ >[gi|1765875|dbj|BAA13619.1|](#) core, env and part of E2/NS1 [Hepatitis C virus]
 Length = 414

Score = 280 bits (717), Expect = 8e-75
 Identities = 142/191 (74%), Positives = 143/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MSTLPKPQ P DVKFPGGGQIV ATRKTSESRQPRG

Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP GRHWAQPGY WPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG

Sbjct: 61 RRQPIPKARQPTGRHWAQPGYAWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDT+TCGFADLMGYI R IEDGINYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTITCGFADLMGYIPVLGAPLGGVAAALAHGVRIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA

Sbjct: 181 LLSCLTTPASA 191

☐ >[gi|2252490|emb|CAA72338.1|](#) HCV polyprotein [Hepatitis C virus type 4a]
 Length = 3008

Score = 280 bits (717), Expect = 9e-75
 Identities = 138/191 (72%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG

Sbjct: 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGPNDPR RSRNLG

Sbjct: 61 RRQPIPKARRPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRGRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPVGSVARALAHGVRALEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191

LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >gi|3550759|dbj|BAA32664.1| polyprotein [Hepatitis C virus]
Length = 3019

Score = 280 bits (716), Expect = 1e-74
Identities = 138/191 (72%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTLPKPQKRKTNRNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR QGR W QPGYPWPLYGNEGCGWAGWL+SPRGSRP WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARPSQGRTWGQPGYPWPLYGNEGCGWAGWLMSPRGSRPSWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCG ADLMGYI RAIEDGINYATGNLPGCSFSIF+LA
Sbjct: 121 KVIDTLTCGLADLMGYIPVVGGPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFILA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|1765881|dbj|BAA13622.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 280 bits (716), Expect = 1e-74
Identities = 141/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTLPKPQKRKTNRNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWL+SPRGSRPHWGPNDPR RSRNLG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLMSPRGSRPHWGPNDPRHRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R IEDGINYATGNLPGCSFSIF LA
Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRIEDGINYATGNLPGCSFSIFFLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|7650248|gb|AAF65955.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 280 bits (715), Expect = 1e-74
Identities = 137/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP+WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|464178|dbj|BAA03581.1| polyprotein [Hepatitis C virus]
Length = 3011

Score = 279 bits (714), Expect = 2e-74
Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRVGVVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP+DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGSPDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >gi|1765885|dbj|BAA13624.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 279 bits (714), Expect = 2e-74
Identities = 142/191 (74%), Positives = 145/191 (75%)

Query: 1 MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPPKQ P DVKFPGGG+IV ATRKTSERSQPRG
Sbjct: 1 MSTLPPKQRKTKRNTYRRPMDVKFPGGGKIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI RA+EDGIN+ATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAFAHGVRALEDGINFATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|1765879|dbj|BAA13621.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 279 bits (713), Expect = 2e-74
Identities = 142/191 (74%), Positives = 144/191 (75%)

Query: 1 MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPPKQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTLPPKQRTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP GRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQPTGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDT+TCG ADLMGYI RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTITCGVADLMGYIPVLGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|1765887|dbj|BAA13625.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 279 bits (713), Expect = 3e-74
Identities = 142/191 (74%), Positives = 144/191 (75%)

Query: 1 MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPPKQ P D+KFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTLPPKQRTKRNTNRRPMDIKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAAFAGHGVRALEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTP SA
Sbjct: 181 LLSCLTTPSA 191

☐ >gi|7650256|gb|AAF65959.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 278 bits (712), Expect = 3e-74

Identities = 137/191 (71%), Positives = 141/191 (73%)

```
Query: 1  MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MST PKPQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPKLGVRATRKTSESRQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP+DPRRRSRNLG
Sbjct: 61  RRQPIPKARQPEGRSWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPSPDRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDTLTCGFADLMGYI                      RA+EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRAVEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191
```

☐ >[gi|482138|pir||S40770](#) genome polyprotein - hepatitis C virus
[gi|221587|dbj|BAA01582.1|](#) polyprotein precursor [Hepatitis C virus]
Length = 3011

Score = 278 bits (712), Expect = 4e-74
Identities = 135/191 (70%), Positives = 140/191 (73%)

```
Query: 1  MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MST+PKPQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTIPKPKRQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPK R+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61  RRQPIPKVRRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDTLTCGFADLMGYI                      R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191
```

☐ >[gi|2327073|gb|AAB67037.1|](#) polyprotein [Hepatitis C virus strain H77]
Length = 3011

Score = 278 bits (711), Expect = 4e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

```
Query: 1  MSTLPPKQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
          MST PKPQ                      P DVKFPGGGQIV                      ATRKTSESRQPRG
Sbjct: 1  MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61  RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
```

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >[gi|471117|dbj|BAA01728.1|](#) polyprotein precursor [Hepatitis C virus]
Length = 3010

Score = 278 bits (711), Expect = 4e-74
Identities = 137/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI RA+EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGAARALAHGVRALEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

☐ >[gi|130461|sp|P27958|POLG_HCVH](#) Genome polyprotein [Contains: Capsid protein C (C
(P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope
glycoprotein E2 (GP68) (GP70) (NS1); Protein P7;
Nonstructural protein NS2 (P21) ; Protease/helicase NS3
(P70) (Hepacivirin) ; Nonstructural protein NS4A (P4);
Nonstructural protein NS4B (P27); Nonstructural protein
NS5A (P56); Nonstructural protein NS5B (P66) (P70)
(RNA-directed RNA polymerase)]
[gi|74464|pir||GNWVCH](#) genome polyprotein - hepatitis C virus (strain H)
[gi|329738|gb|AAA45534.1|](#) polyprotein
Length = 3011

Score = 278 bits (711), Expect = 4e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA

Sbjct: 181 LLSCLTVPASA 191

☐ >[gi|8926245|gb|AAF81759.1|](#) polyprotein [Hepatitis C virus]
Length = 3011

Score = 278 bits (711), Expect = 4e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >[gi|130455|sp|P26664|POLG HCV1](#) Genome polyprotein [Contains: Capsid protein C (C (P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) ; Protease/helicase NS3 (P70) (Hepacivirin) ; Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P66) (P70) (RNA-directed RNA polymerase)]
[gi|74463|pir||GNWVC3](#) genome polyprotein - hepatitis C virus (strain HCV-1)
[gi|329874|gb|AAA45676.1|](#) HCV-1
Length = 3011

Score = 278 bits (711), Expect = 4e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQKKNRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >gi|14532245|gb|AAK66554.1| HCV type 1a/1b chimera polyprotein [synthetic constr
gi|14532247|gb|AAK66555.1| HCV type 1a polyprotein [synthetic construct]
gi|14532249|gb|AAK66556.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >gi|2327071|gb|AAB67036.1| polyprotein [Hepatitis C virus strain H77]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >gi|22129793|ref|NP_671491.1| polyprotein [Hepatitis C virus]
gi|2316098|gb|AAB66324.1| polyprotein [Hepatitis C virus]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >[gi|14532251|gb|AAK66557.1|](#) HCV type 1a/1b chimera mutant polyprotein [synthetic]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

☐ >[gi|2327075|gb|AAB67038.1|](#) polyprotein [Hepatitis C virus strain H77]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTVPASA 191

☐ >gi|9930557|gb|AAG02099.1| polyprotein [Hepatitis C virus]
 Length = 3011

Score = .278 bits (710), Expect = 5e-74
 Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTVPASA 191

☐ >gi|3098655|gb|AAC15732.1| polyprotein [Hepatitis C virus]
 Length = 2864

Score = 277 bits (709), Expect = 6e-74
 Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGLWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTIPASA 191

☐ >gi|15529111|gb|AAK97744.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (709), Expect = 6e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVVEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

☐ >gi|1944376|dbj|BAA19625.1| unnamed protein product [Hepatitis C virus]
Length = 3010

Score = 277 bits (709), Expect = 7e-74
Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP+WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGGMWAGWLLSPRGSRPNWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|1009261|dbj|BAA07091.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 277 bits (709), Expect = 7e-74
Identities = 142/191 (74%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Sbjct: 61 RRQPIPKAR GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI RAIEDGINYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA

Sbjct: 181 LLSCLTTPASA 191

☐ >gi|3098644|gb|AAC15727.1| polyprotein [Hepatitis C virus]
 Length = 2864

Score = 277 bits (709), Expect = 7e-74
 Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG

Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG

Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLT PASA

Sbjct: 181 LLSCLTIPASA 191

☐ >gi|5918961|gb|AAD56196.1| polyprotein [Hepatitis C virus]
 Length = 3010

Score = 277 bits (709), Expect = 8e-74
 Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG

Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP+DPRRRSRNLG

Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGSPDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADL+GYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLLGYIPLVGAPIGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA

Sbjct: 181 LLSCLTTPASA 191

☐ >gi|2943784|dbj|BAA25076.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 8e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

```
Query: 1  MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
          MST PKPQ                      P DVKFPGGGQIV                      ATRKTSEERSQPRG
Sbjct: 1  MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKAR+P+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGPNDPRRRSRNLG
Sbjct: 61  RRQPIPKARRPEGRTWAQPGYPWPLYGNEGLWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDTLTCGFADLMGYI                      R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191
```

☐ >gi|7650246|gb|AAF65954.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 8e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

```
Query: 1  MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
          MST PKPQ                      P DVKFPGGGQIV                      ATRKTSEERSQPRG
Sbjct: 1  MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61  RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
          RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61  RRQPIPKARQPEGRAWAQPGYPWPLYGNEGLWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
          KVIDTLTCGFADLMGYI                      R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
          LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191
```

☐ >gi|7650240|gb|AAF65951.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 9e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

```
Query: 1  MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
          MST PKPQ                      P DVKFPGGGQIV                      ATRKTSEERSQPRG
Sbjct: 1  MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60
```

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTIPASA 191

☐ >gi|5420377|emb|CAB46677.1| polyprotein [Hepatitis C virus type 1b]
 Length = 3010

Score = 277 bits (708), Expect = 9e-74
 Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTIPASA 191

☐ >gi|5918963|gb|AAD56197.1| polyprotein [Hepatitis C virus]
 Length = 3010

Score = 277 bits (708), Expect = 9e-74
 Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP+DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGSPDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADL+GYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLLGYIPLVGAPIGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
 LLSCLTTPASA

Sbjct: 181 LLSCLTTPASA 191

☐ >gi|7650244|gb|AAF65953.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 9e-74
Identities = 137/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLS LTPASA
Sbjct: 181 LLSGLTTPASA 191

☐ >gi|7650224|gb|AAF65943.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPK RQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKVRQPEGRTWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARVLAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|7650234|gb|AAF65948.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60

MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60
 Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
 Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
 Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTVPASA 191

☐ >gi|7341103|gb|AAF61205.1| polyprotein [Hepatitis C virus]
 Length = 3008

Score = 276 bits (707), Expect = 1e-73
 Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60
 Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP+WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGMWAGWLLSPRGSRPNWGPTDPRRRSRNLG 120
 Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
 Query: 181 LLSCLTTPASA 191
 LLSCLT PASA
 Sbjct: 181 LLSCLTIPASA 191

☐ >gi|1814086|dbj|BAA09072.1| polyprotein [Hepatitis C virus]
 Length = 3010

Score = 276 bits (707), Expect = 1e-73
 Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSESRQPRG 60
 MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
 Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60
 Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
 Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
 Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
 KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
 Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGASRALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

☐ >[gi|7650252|gb|AAF65957.1|](#) polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (707), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +ED +NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGARALAHGVRVLEDSVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >[gi|1814089|dbj|BAA09076.1|](#) polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (707), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXATRKTSEERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSEERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGASRALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

☐ >[gi|1765868|dbj|BAA13615.1|](#) core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 276 bits (706), Expect = 1e-73
Identities = 140/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP GR W QPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQPTGRSWGQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCG ADLMGYI RAIEDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGLADLMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|1009263|dbj|BAA07092.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 276 bits (706), Expect = 1e-73
Identities = 141/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLRRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARHQTGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRALEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

☐ >gi|7650226|gb|AAF65944.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (706), Expect = 2e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191

LLSCLT PASA

Sbjct: 181 LLSCLTIPASA 191

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: May 11, 2004 12:59 AM

Number of letters in database: 593,787,773

Number of sequences in database: 1,798,171

Lambda	K	H
0.320	0.140	0.471

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 42,029,332

Number of Sequences: 1798171

Number of extensions: 1637745

Number of successful extensions: 3615

Number of sequences better than 10.0: 298

Number of HSP's better than 10.0 without gapping: 294

Number of HSP's successfully gapped in prelim test: 4

Number of HSP's that attempted gapping in prelim test: 3029

Number of HSP's gapped (non-prelim): 302

length of query: 191

length of database: 593,787,773

effective HSP length: 118

effective length of query: 73

effective length of database: 381,603,595

effective search space: 27857062435

effective search space used: 27857062435

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 70 (31.6 bits)